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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
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EXAMINER	
HADDAD, MAHER M	
ART UNIT	**PAPER NUMBER**
1644	

DATE MAILED: 09/27/2005

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	10/785,220	ASHKENAZI ET AL.	
	Examiner	Art Unit	
	Maher M. Haddad	1644	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *24 February 2004*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *49-63* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *49-63* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date *6/07/04&4/18/05*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☒ Other: *Sequence alignment*.

DETAILED ACTION

1. Claims 49-63 are pending.

2. Applicant's election without traverse of Group II, claims 49-63 as they read on an isolated nucleic acid molecule of SEQ ID NO: 11, vectors, host cells, and a process of producing the polypeptide filed on 4/22/05, is acknowledged.

In view of Applicant's remarks that there was an error in the previous sequence listing in that the sequence rightly submitted as SEQ ID NO: 7 was erroneously further repeated as SEQ ID NO:11. The correct sequence for SEQ ID NO: 11 should be that disclosed in Fig. 5 of the instant application. The Examiner extends the search to cover Group I (claims 49-63).

3. Claims 49-63 are under examination as they read on an isolated nucleic acid molecule of SEQ ID NO: 11 encoding SEQ ID NO:1, vectors, host cells, and a process of producing the polypeptide.

4. Applicant's IDS, filed 4/18/05 & 6/7/04, is acknowledged. Only the references initiated, IDS file 6/7/04, were found in the parent applications 09/953,499 and 09/254,465. The BLAST results provided as reference Nos. 15-17 are not appropriate for an IDS. BLAST alignments should be appended as part of each individual sequence reference, which must include the Accession No., Database and earliest available date of the reference sequence in order to be appropriate for inclusion in the IDS. Further reference C1, filed 4/18/05, was crossed out because it is a duplicate of reference 210 filed on 6/7/04.

5. Claim 62 is objected to for the citation "the host cell Claim 63". It is suggested that the claim be amended to recite "the host cell of Claim 61".

6. Claim 52 is objected to for the following informality: the "ca" should be changed to "a". Correction is required.

7. The amendment filed 8/22/05 is objected to under 35 U.S.C. 132 because it introduces new matter into the disclosure. 35 U.S.C. 132 states that no amendment shall introduce new matter into the disclosure of the invention. The added material which is not supported by the original disclosure is as follows:

The preliminary amendment filed on 8/22/05 to the sequence listing substituting of Figure 5 (SEQ ID NO: 11) with the current SEQ ID NO: 11 represents a departure from the specification and the claims as originally filed. Applicant points out the there was an error in pervious sequence listing in that, the sequence rightly submitted as SEQ ID NO: 7 was erroneously further repeated as SEQ ID NO:11. However, Figure 5 depicts nucleic acid position No. 1306 as C, the

SEQ ID NO: 11 now lists the nucleic acid 1306 as A. Furthermore, the instant SEQ ID NO: 11 has different N-terminal nucleotides that are not as those depicted in Fig. 5. The specification and the claims as originally filed have no support for the new nucleic acid substitution as listed in SEQ ID NO: 11.

Applicant is required to cancel the new matter in the response to this Office action.

8. The following is a quotation of the second paragraph of 35 U.S.C. 112.

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

9. Claims 53, 58 and 63 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

A) Claims 53, 58, and 63 are indefinite in the recitation of "PRO301" because its characteristics are not known. The use of "PRO301" polypeptide as the sole means of identifying the claimed polypeptide renders the claim indefinite because "PRO301" is merely a laboratory designation which does not clearly define the claimed product, since different laboratories may use the same laboratory designation to define completely distinct polypeptide. It is suggested that the SEQ ID NO: 1 be cited in the claims.

10. The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

11. Claims 49-63 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. This is a New Matter rejection.

The sequence "SEQ ID NO: 11" claimed in claims 49, 53 and 59 represents a departure from the specification and the claims as originally filed.

Applicant's amendment filed 8/22/05 and 4/22/05 points to the Figure 5 for support for the newly claimed SEQ ID NO: 11 as claimed in claims 49, 53 and 59. However, the Figure 5 does not provide a clear support of "SEQ ID NO:11" because the claimed SEQ ID NO: 11 substituted nucleic acid C at position 1306 of Figure 5 with the nucleic acid A. Furthermore, the N-terminal nucleotides of the new SEQ ID NO: 11 do not correspond to the sequence depicted in Fig. 5. The

instant claims now recite a limitation which was not clearly disclosed in the specification and recited in the claims as originally filed.

12. Claims 49-63 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention.

It is apparent that the pRK5-based plasmid DNA40628-1216 is required to practice the claimed invention. As a required element, it must be known and readily available to the public or obtainable by a repeatable method set forth in the specification. If it is not so obtainable or available, the enablement requirements of 35 USC 112, a deposit of the plasmid, may satisfy first paragraph. See 37 CFR 1.801-1.809.

The amendment to the specification on page 68, filed 2/24/04, to assure that "all restrictions imposed by the depositor on the availability to the public of the deposited material will be irrevocably removed upon the granting of a patent, is acknowledged. However, in order to be fully compliant with the requirement, applicants must state that the deposit will be maintained for a term of at lest 30 years *and at least five (5) years after the most recent request for the furnishing of a sample of the deposit was received by the depository.* See 37 C.F.R. 1.806.

13. Claims 49-53 and 59-63 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for an isolated nucleic acid sequence of SEQ ID NO: 11 encoding SEQ ID NO: 1; an isolated nucleic acid sequence encoding SEQ ID NO: 1, a nucleic acid sequence encoding the polypeptide of SEQ I DNO:1 lacking its associated signal sequence for the inhibition of VEGF stimulated proliferation of endothelial cells, does not reasonably provide enablement for any isolated nucleic acid molecule comprising a nucleotide sequence having "at least 95% sequence identity" to (a) a nucleotide sequence encoding the polypeptide of SEQ ID NO:1, (b) a nucleotide sequence encoding the polypeptide of SEQ ID NO:1 lacking its associated signal sequence (c) the nucleic acid of SEQ ID NO:11, (d) the full-length coding sequence of the nucleic acid sequence of SEQ ID NO: 11, or (e) the full-length coding sequence of the cDNA deposited under ATCC accession number 209432 in claim 49, or a process for producing any "PRO301 polypeptide" comprising culturing the host cell of Claim 51 under conditions suitable for expression of said polypeptide and recovering said polypeptide from the cell culture in claim 53, under conditions suitable for expression of said polypeptide and recovering said polypeptide from the cell culture in claim 58, an isolated nucleic acid molecule that hybridizes under the specific stringent conditions to a complement of (a) a nucleic acid molecule encoding the polypeptide of SEQ ID NO :1, (b) a complement of a nucleotide sequence encoding the polypeptide of SEQ ID NO:1 lacking its associated signal, (c) a complement of the nucleic acid sequence of SEQ ID NO:11, (d) a complement of the full-length coding sequence of the nucleic acid sequence of SEQ ID NO: 11, or (e) a complement of the full-length coding sequence of the nucleic acid sequence of SEQ ID NO:11, or (e) a complement of the full-length coding sequence of the cDNA deposited under ATCC accession number 209432 in claim 59 or a

process for producing a PRO301 polypeptide comprising culturing the host cell of Claim 61 under conditions suitable for expression of said polypeptide and recovering said polypeptide from the cell culture in claim 63. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the invention commensurate in scope with these claims.

Factors to be considered in determining whether undue experimentation is required to practice the claimed invention are summarized *In re Wands* (858 F2d 731, 737, 8 USPQ2d 1400, 1404 (Fed. Cir. 1988)). The factors most relevant to this rejection are the scope of the claim, the amount of direction or guidance provided, the lack of sufficient working examples, the unpredictability in the art and the amount of experimentation required to enable one of skill in the art to practice the claimed invention.

The claims are directed to isolated nucleic acids having at least 95% sequence identity to SEQ ID NO: 11, a nucleotide sequence encoding the polypeptide of SEQ ID NO:1 with or without its signal peptide. Further the claims are directed to a nucleic acid molecule that hybridizes under specific stringent conditions to SEQ ID NO: 1 encoding SEQ ID NO:11 with or without the signal sequence. Dependent claims are directed to vectors, host cells comprising the isolated nucleic acids and process of producing the polypeptide.

The claimed nucleic acids are described at least in part in terms of the protein that might be encoded, the scope of the protein itself must be considered: The specification discloses that PRO301 A33 antigen (see Figure 1, and page 1, lines 36-37). Further the specification, on page 7, lines 39-40 discloses that the PRO301 polypeptide is 299 amino acids long, having signal sequence at residue 1-27, and extracellular domain at residue 28-235, Ig superfamily homology at residue 94-235, a potential transmembrane domain at residue 236-258, and an intracellular domain at about residue 259-299. The specification on page 53, under example 4, discloses the use of the protein of SEQ ID NO:1 in the inhibition of VEGF stimulated proliferation of endothelial cells growth.

The claims encompass an unreasonable number of inoperative polynucleotides, which the skilled artisan would not know how to use. There are no working examples of nucleic acids less than 100% identical to SEQ ID NO:11. The specification fails to provide guidance for using polypeptides related to (i.e. at least 95% identity) but not identical to SEQ ID NO:1 that share the ability to inhibit endothelial cell growth of the encoded polypeptide of SEQ ID NO:1, other than the nucleic acid of SEQ ID NO:11 encoding SEQ ID NO:1. The claims are broad because they do not require the claimed nucleic acid to encode a polypeptide identical to the disclosed sequence and because the claims have no functional limitation.

The art acknowledges that function cannot be predicted based solely on structural similarity to a protein found in the sequence databases and recognized that it was unpredictable if any functional activity will be shared by two polypeptides having less than 100% identity over the full length of their sequences. Attwood (Science 2000; 290:471-473) teaches that "[i]t is presumptuous to make functional assignments merely on the basis of some degree of similarity

between sequences. Similarly, Skolnick et al. (Trends in Biotech. 2000; 18(1):34-39) teach that the skilled artisan is well aware that assigning functional activities for any particular protein or protein family based upon sequence homology is inaccurate, in part because of the multifunctional nature of proteins (e.g., "Abstract" and "Sequence-based approaches to function prediction", page 34). Even in situations where there is some confidence of a similar overall structure between two proteins, only experimental research can confirm the artisan's best guess as to the function of the structurally related protein (see in particular "Abstract" and Box 2). Thus it is unpredictable if any functional activity will be shared by two polypeptides having less than 100% identity over the full length of their sequences.

Claim 59 recites nucleic acid molecules that hybridize to the recited sequences. The term "hybridize" or "hybridization" generically refers to a process in which a strand of nucleic acid joins or matches up with a complementary strand through the process of base pairing, wherein the process is basically used to locate or identify DNAs encoding specific proteins. It is well established in the art that 15-20 bases have been considered sufficient to achieve this process. The breadth of the claims includes nucleic acids of as little as 10 nucleotides. With these points in mind, it is the Examiner's position that given the claims their broadest reasonable interpretation, this language reads on an infinite number of possible DNA sequences for which there is not sufficient enablement.

The Examples provided in the specification do not provide a representative number of different DNA sequences that would enable a representative number of the above discussed DNA sequences with assurances that they possess or encode proteins having the desired activity, or alternatively can be used as probes or primers for the purpose of amplifying or detecting the PRO301 gene. The mere recitation of this term, and the definitions provided do not serve as sufficient guidance to enable the breadth of the claims for the various DNA sequences claimed. See Ex parte Forman, 230 USPQ 546. Since the first paragraph of the statute under 35 U.S.C 112 requires that there must be an enabling disclosure to support the breadth of the claims, a review of the specification confirms that the scope of the various DNA sequences that are discussed above have not been enabled. There is but a single nucleic acid disclosed with reference to PRO301, SEQ ID NO: 11. In the absence of sufficient guidance, it would require undue experimentation to enable a commensurate number of the sequences that are encompassed by the claims.

Reasonable correlation must exist between the scope of the claims and scope of enablement set forth. Without sufficient guidance, the changes which can be made in the instantly recited nucleic acid sequence is unpredictable, as is the identity of which subsequences would hybridize to SEQ ID NO:11 encoding SEQ ID NO: 1 with or without signal sequence; thus the experimentation left to those skilled in the art is unnecessarily, and improperly, extensive and undue.

14. Claims 49-53 and 59-63 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably

convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

Applicant is in possession of an isolated nucleic acid sequence of SEQ ID NO: 11 encoding SEQ ID NO: 1; an isolated nucleic acid sequence encoding SEQ ID NO: 1, a nucleic acid sequence encoding the polypeptide of SEQ I DNO:1 lacking its associated signal sequence for the inhibition of VEGF stimulated proliferation of endothelial cells.

Applicant is not in possession of any isolated nucleic acid molecule having "at least 95% sequence identity" to (a) a nucleotide sequence encoding the polypeptide of SEQ ID NO:1, (b) a nucleotide sequence encoding the polypeptide of SEQ ID NO:1 lacking its associated signal sequence (c) the nucleic acid of SEQ ID NO:11, (d) the full-length coding sequence of the nucleic acid sequence of SEQ ID NO: 11, or (e) the full-length coding sequence of the cDNA deposited under ATCC accession number 209432 in claim 49, or a process for producing any "PRO301 polypeptide" comprising culturing the host cell of Claim 51 under conditions suitable for expression of said polypeptide and recovering said polypeptide from the cell culture in claim 53, under conditions suitable for expression of said polypeptide and recovering said polypeptide from the cell culture in claim 58, an isolated nucleic acid molecule that hybridizes under the specific stringent conditions to a complement of (a) a nucleic acid molecule encoding the polypeptide of SEQ ID NO :1, (b) a complement of a nucleotide sequence encoding the polypeptide of SEQ ID NO:1 lacking its associated signal, (c) a complement of the nucleic acid sequence of SEQ ID NO:11, (d) a complement of the full-length coding sequence of the nucleic acid sequence of SEQ ID NO: 11, or (e) a complement of the full-length coding sequence of the nucleic acid sequence of SEQ ID NO:11, or (e) a complement of the full-length coding sequence of the cDNA deposited under ATCC accession number 209432 in claim 59 or a process for producing a PRO301 polypeptide comprising culturing the host cell of Claim 61 under conditions suitable for expression of said polypeptide and recovering said polypeptide from the cell culture in claim 63.

Applicant has disclosed only nucleic acid of SEQ ID NO: 11 encoding SEQ ID NO:1 with or with out signal sequence and a nucleotide sequence encoding the polypeptide of SEQ ID NO:1; therefore, the skilled artisan cannot envision all the contemplated nucleic acid sequence possibilities recited in the instant claims. Consequently, conception cannot be achieved until a representative description of the structural and functional properties of the claimed invention has occurred, regardless of the complexity or simplicity of the method. Adequate written description requires more than a mere statement that it is part of the invention. See *Fiers v. Revel*, 25 USPQ2d 1601, 1606 (CAFC1993). The Guidelines for the Examination of Patent Application Under the 35 U.S.C.112, ¶ 1"Written Description" Requirement make clear that the written description requirement for a claimed genus may be satisfied through sufficient description of a representative number of species disclosure of relevant, identifying characteristics, i.e., structure or other physical and or chemical properties, by functional characteristics coupled with a known or disclosed correlation between function and structure, or by a combination of such identifying characteristics, sufficient to show the applicant was in possession of the genus (Federal Register, Vol. 66, No. 4, pages 1099-1111, Friday January 5, 20001, see especially page 1106 3rd column).

Vas-Cath Inc. v. Mahurkar, 19 USPQ2d 1111, makes clear that "applicant must convey with reasonable clarity to those skilled in the art that, as of the filing date sought, he or she was in possession of the invention. The invention is, for purposes of the written description inquiry, whatever is now claimed." (See page 1117.) The specification does not "clearly allow persons of ordinary skill in the art to recognize that [he or she] invented what is claimed." (See Vas-Cath at page 1116.). Consequently, Applicant was not in possession of the instant claimed invention. See University of California v. Eli Lilly and Co. 43 USPQ2d 1398.

Applicant is directed to the final Guidelines for the Examination of Patent Applications Under the 35 U.S.C. 112, ¶ 1 "Written Description" Requirement, Federal Register, Vol. 66, No. 4, pages 1099-1111, Friday January 5, 2001.

16. The priority is set at 11/20/1998 for the claimed nucleic acid because the utility for the encoded protein is active in the inhibition of VEGF stimulated proliferation of endothelial cells. The earliest disclosure of this result that can be confirmed by the Examiner is in the PCT/US98/24855. Accordingly, the rejections below base on the Examiner's determination of the priority date.

17. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless --

(e2) the invention was described in a patent granted on an application for patent by another filed in the United States before the invention thereof by the applicant for patent, or on an international application by another who has fulfilled the requirements of paragraphs (1), (2), and (4) of section 371(c) of this title before the invention thereof by the applicant for patent.

The changes made to 35 U.S.C. 102(e) by the American Inventors Protection Act of 1999 (AIPA) and the Intellectual Property and High Technology Technical Amendments Act of 2002 do not apply when the reference is a U.S. patent resulting directly or indirectly from an international application filed before November 29, 2000. Therefore, the prior art date of the reference is determined under 35 U.S.C. 102(e) prior to the amendment by the AIPA (pre-AIPA 35 U.S.C. 102(e)).

16. Claims 49-63 are rejected under 35 U.S.C. 102(e) as being anticipated by U.S. Pat. No. 6,358,707, as is evidenced by the specification on page 49, lines 36-40.

The `707 patent teaches and claims the full length coding sequence of the nucleic acid (patented SEQ ID NO: 1) having 100% sequence identity to the claimed SEQ ID NO: 11 encoding a polypeptide (patented SEQ ID NO: 2) that has 100% sequence identity to claimed SEQ ID NO:1 (see patented SEQ ID NOs: 1 and 2 and claims 1-10 in particular). Further the `707 patent teaches an expression vector comprising the polynucleotide of SEQ ID NO:1 and a host cell comprising the expression vector. Also, the `707 teaches a process for producing a polypeptide of claimed SEQ ID NO:1 (patented SEQ ID NO: 1) comprising culturing the host cell comprising the expression vector which comprises claimed SEQ ID NO: 11 (patented SEQ ID

NO: 1) and recovering the polypeptide from the culture. In addition, the '707 patent teaches representative examples of appropriate hosts include E. coli, yeast cells, Bacillus cells, insect cells or CHO cells (see col., 7, lines 4-10 in particular). Finally, the '707 teaches polynucleotides which are identical or sufficiently identical to a nucleotide sequence contained in SEQ ID NO:1, can be used as hybridization probes for cDNA and genomic DNA or as primers for a nucleic acid amplification (PCR) reaction. Given that the patented nucleic acid molecule has 100% sequence identity to the full-length coding sequence of the nucleic acid sequence of SEQ ID NO: 11, the referenced nucleic acid molecule would hybridized under the recited stringent conditions to the a complement of a nucleic acid molecule encoding the polypeptide of claimed SEQ ID NO:1 with or without the associated signal sequence, a complement of the nucleic acid sequence of claimed SEQ ID NO: 11, a complement of the full-length coding sequence of the nucleic acid sequence of claimed SEQ ID NO: 11 or a complement of the full-length coding sequence of the cDNA deposited under ATCC accession number, as is evidenced by the specification on page 49, lines 36-40, that SEQ ID NO: 11 is the cDNA sequence deposited under ATCC accession number 209432 encodes the PRO301 polypeptide of SEQ ID NO:1.

The reference teachings anticipate the claimed invention.

14. The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

(a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(f) or (g) prior art under 35 U.S.C. 103(a).

15. Claims 49-63 are rejected under 35 U.S.C. 103(a) as being unpatentable over Naik *et al* (1995), as is evidenced by Sobocka et al, in view of Alberts *et al* (1989).

Naik *et al* teach a novel platelet receptor, F11antigen. Also, Naik *et al* teach that the N-terminal 26 amino acid sequences of the F11 antigen, which has 32 and 35 kDa protein, were identical and contained a single unblocked serine in the N-terminal position. Further, when digested with N-glycanase, the 32 and 35 kDa proteins were converted into a single ~29 kDa protein, indicating that these two proteins are derived from the same core protein but differ in their degree of glycosylation. Also, Naik *et al* teach that the internal amino acid sequence analysis of

the F11 antigen provided information concerning 68 amino acids and suggested two consensus phosphorylation sites for protein kinase C (PKC) (see abstract, page 159, 2nd col., 2nd paragraph, and page 160, 2nd col., 1st paragraph in particular). While Naik *et al* is silence with respect to SEQ ID NO: 1, referenced F11 antigen is the claimed SEQ ID NO: 1 as is evidenced by Sobocka *et al* that the reported sequence of human homologue of JAM (claimed SEQ ID NO: 1, see attached sequence alignment in particular) by Martin-Padura et al and Ozaki et al, is identical to the sequence of the human platelet F11R (see page 2607, 1st col., end of the 1st paragraph). Applicant's disclosure of SEQ ID NO:1 is mainly further characterization of otherwise old product.

The claimed invention differs from the reference teachings only by the recitation of nucleic acid molecule comprising a nucleotide sequence encoding the polypeptide of SEQ ID NO:1 in claims 49 and 54, or a nucleic acid molecule that hybridizes under stringent conditions to a complement of a nucleic acid molecule encoding the polypeptide of SEQ ID NO: 1 with or without its associated signal sequence in claim 59, a vector in claims 50, 55 and 60, a host cell in claims 51, 56 and 61, a yeast cell in claims 52, 57 and 62, a process for producing the polypeptide in claims 53, 58 and 63.

Alberts *et al* teach once a protein has been purified to homogeneity, its biological activities can be examined in detail. A small part of the protein's amino acid sequence can be determined and its gene can be cloned; the remaining amino acid sequence is then obtained from the nucleotide sequence of the gene (page 174, under Summary in particular). Further, Alberts *et al* teach genetic engineering techniques using selecting regions of a known amino acid sequence to make synthetic oligonucleotide probes to identify the clones of interest in a DNA library (see page 262, 3rd paragraph and Fig. 5-84 in particular). Further, Alberts *et al* teach the recombinant DNA technology has revolutionized the study of the cell. Any region of a cell's DNA can now be excised with restriction nucleoases and inserted into a self-replicating genetic element (a plasmid) to produce a "genomic DNA clone". Unlimited amounts of a highly purified DNA molecule can thereby be obtained and its nucleotide sequence determined at a rate of hundreds of nucleotides per day, revealing the amino acid sequence of the protein it encodes. Further, the consequences of recombinant DNA technology are far-reaching in other ways as well. Bacteria, yeasts, or mammalian cells can be engineered to synthesize any desired protein in large quantities, making it possible to analyze the structure and function of the protein in detail, or to use the protein as a drug or a vaccine for medical purposes (see page 196 under Summary in particular). Finally, Alberts et al teaches expression vector allow cDNA clones to be sued to overproduce proteins by means of genetic engineering, bacteria, yeast or mammalian cells can be induced to make vast quantities of useful protein. For example bacterial cells with plasmids vectors that have been engineered in this way are especially adept at protein production (see page 265, 2nd paragraph in particular).

The resultant nucleic acid would hybridize to the complement of a nucleic acid molecule encoding the polypeptide of SEQ ID NO:1 with or without it's the signal sequence.

It would have been obvious to one of ordinary skill in the art at the time the invention was made to determine the rest of the F11R amino acid sequence taught by Naik *et al* using the genetic engineering techniques and its gene can be cloned express the DNA using the vectors, host cells and the method of producing the polypeptide as taught by Albert *et al.*

One of ordinary skill in the art at the time the invention was made would have been motivated to do so because bacteria, yeasts, or mammalian cells can be engineered to synthesize any desired protein in large quantities, making it possible to analyze the structure and function of the protein in detail, or to use the protein as a drug or a vaccine for medical purposes as taught by Alberts *et al.*

From the combined teachings of the references, it is apparent that one of ordinary skill in the art would have had a reasonable expectation of success in producing the claimed invention. Therefore, the invention as a whole was *prima facie* obvious to one of ordinary skill in the art at the time the invention was made, as evidenced by the references, especially in the absence of evidence to the contrary.

16. No claim is allowed.

17. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Maher Haddad whose telephone number is (571) 272-0845. The examiner can normally be reached Monday through Friday from 7:30 am to 4:00 pm. A message may be left on the examiner's voice mail service. If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Christina Chan can be reached on (571) 272-0841. The fax number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

September 15, 2005

Maher Haddad

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